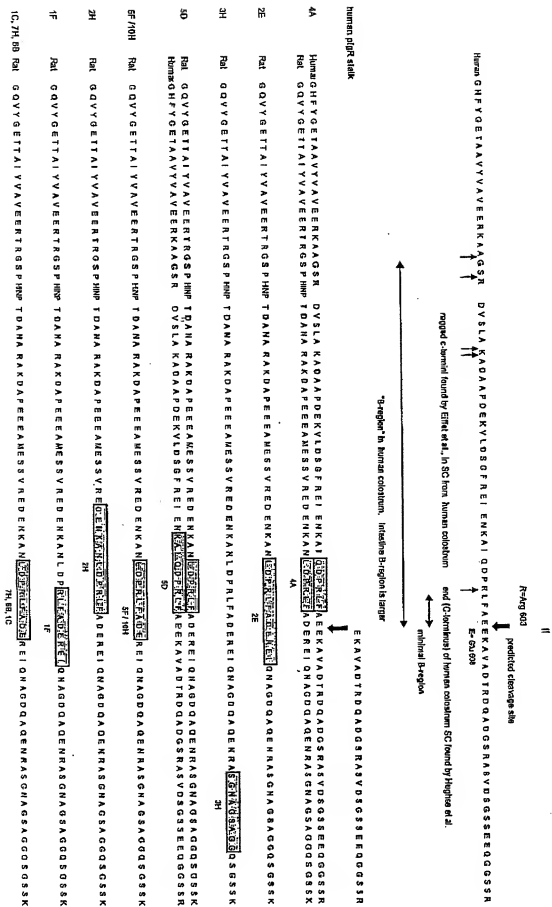


[illegible]

Figure 1

10	20	30	40	50	60
MLLFVLTCLL	AVFPAISTKS	PIPGPEEVNS	VEGNSVSITC	YYPPTSUNRH	TRKYWCRQGA
70	80	90	100	110	120
RGGCITLISS	EGYVSSKYAG	RANLTNFPEN	GTFVVNIAQL	SQDDSGRYKC	GLGINSRGLS
130	140	150	160	170	180
FDVSLEVSQG	PGLLNDTKVY	TVDLGRVTI	NCPPKTENAQ	KRKSLYKQIG	LYPVLVIDSS
190	200	210	220	230	240
GVVNPNYIGR	IRLDIQGTGQ	LLFSVVINQL	RLSDAGQYLC	QAGDSDSNK	KVADLQVLKP
250	260	270	280	290	300
EPELVYEDLR	GSVTFHCALG	PEVANVAKFL	CRQSSGENCD	VVNTLKGRA	PAFEGRILLN
310	320	330	340	350	360
PQOKDGSFSV	VITGLRKEDA	GRYLCGAHSD	GQLQEGSPIC	AWQLFVNES	TIPRSPITVVK
370	380	390	400	410	420
GVAGSSVAVL	CPYNRKESKS	IKYWCLWEGA	QNGRCPLLD	SEGWVKAQYE	GRSLLEEPG
430	440	450	460	470	480
NGTFIVILNQ	LTSRDAGFYW	CLTNGDTLWR	TIVEIKIIEG	EPNLKVPGNV	TAVLGETILKV
490	500	510	520	530	540
PCHFPCFKFS	YEKYWCKWRN	TGCQALPSQD	EGPSKAFVNC	DENSRLVSLT	LNLVTRADEG
550	560	570	580	590	600
WYWCVGKQGH	FYGETAAVYV	AVEERKAAGS	RDVSLAKADA	APDEKVLD SG	FREIENKAIQ
610	620	630	640	650	660
DPRLFAEKA	VADTRDQADG	SRASVDSGSS	EEQGGSSRAL	VSTLVPLGLV	LAVGAVAVGV
670	680	690	700	710	720
ARARHRKQVD	RVSIRSYRTD	ISMDFENS	EFGANDNMGA	SSITQETSLG	GKEEFVATTE
730	740	750	760		
STTETKEPKK	AKRSSKEEAE	MAYKDFLLQS	STVAASAQDG	PQEA	

Figure 2



Pelb/4AF/myc/6HIS

PelB leader		FLAG	Heavy chain FR 1		CDR 1
MKYLLPTAAAGLLILIAAPAMADYKARQVQLVQSGGGLVQPGSLRLSCAASGFTFSSTAMS					
FR 2	CDR 2		FR 3		
WVRQAPGKGLWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAPEDTA VYYCAR					
CDR 3	FR 4	linker	Light chain FR 1		
SFTVNSGYFQHWGQFTLVTVSSGGGSGGGGGGGSEIVLTQSPSTLSASIGDRVITTCRASEGIYHWILA					
FR 2	CDR 2	FR 3		CDR 3	
WYQQKPGKAPKLLITYKASSIASGVPSPRFGSGSGGTDFITLTISLQPEDFATYYQH YDSTPPT					
FR 4	myc	6 HIS			
EGQGTKVDIKRAAAEQKLISEEDINGAAHHHHHH					

The amino acid sequence of the secreted form of the ScFv 4AF is shown. The ScFv consists of a pelb leader (for secretion in *E. coli*), a FLAG epitope tag, a heavy chain variable region, a linker sequence (GGGS repeated three times), a light chain variable region, a myc epitope tag and a 6HIS tag (for purification by Immobilized Metal-ion Affinity Chromatography (IMAC)). The framework (FR) and complementarity-determining regions (CDR) of the heavy chain and light chain are indicated.

Figure 5